



MALQGISVVELSGLAPGPFCCAMVLADFGARVVRVDRPGSRYDVSR LGRGKRSVLVDLQKPRGA AVLRLRLCK  
RSDV LLEPFRRGVMEKLQLGPEILQRENRLIYARLSGFGQSGSFCLAGHDINYLALSGVLSKIGRSGEN  
PYAPLNL LADFAGGGLMCALGIIMALFDTRTGTGKGQVIDANMVEGTAYLSSFLWKTQKSSLWEAPRGQNM L  
DGGAPFYTTYRTADGEFMAVGAI EPQFYELLIKGLGLKSDLPNQMSMDDWPEMKKKFADVF AKKTKAEWC  
QIFDGTDACVTPVLT FEEVVHHDHNKERGSFITSEEQDVSPRPAPLL LNTPAIPSFKRDPFIGEHTEEILE  
EFGFSREEIYQLNSDKIIESNKVKASL

**FIGURE 2**

FIG. 3

SV1 (AMACR Isoform 1; >Fmhm\_x4226FL01)  
GGGCGCCGGGATTGGGAGGGCTTCTTGCAGGCTGCTGGGCTGGGGCTAAG  
GGCTGCTCAGTTTCTTTCAGCGGGGCACTGGGAAGCGCCATGGCACTGCA  
GGGCATCTCGGTCTGGAGCTGTCCGGCCTGGCCCCGGGCCCCGTTCTGTG  
CTATGGTCTCTGGCTGACTTCCGGGGCGGTGTGGTACGCGTGGACCGGCCC  
GGCTCCCCTACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGT  
GCTGGACCTGAAGCAGCCGCGGGGAGCCGCCGTGCTGCGGCGTCTGTGCA  
AGCGGTTCGGATGTGCTGCTGGAGCCCTTCCGCCGCGGTGTCATGGAGAAA  
CTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAAATCCAAGGCTTATTTA  
TGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTG  
GCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATTGGC  
AGAAGTGGTGAGAAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTTGC  
TGGTGGTGGCCTTATGTGTGCACTGGGCATTATAATGGCTCTTTTTGACC  
GCACACGCACTGGCAAGGGTCAGGTCAATTGATGCAAATATGGTGGAAAGGA  
ACAGCATATTTAAGTTCTTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTG  
GGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTATA  
CGAATTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAA  
CCCCAGTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGA  
ACTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGAAGAAGT  
TTGCAGATGTATTTGCAAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTT  
GACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGT  
TCATCATGATCACAAACAGGAACGGGGCTCGTTTATCACCAGTGAGGAGC  
AGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCAGCCATC  
CCTTCTTTCAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACT  
TGAAGAATTTGGATTACGCCGCGAAGAGATTTATCAGCTTAACTCAGATA  
AAATCATTGAAAGTAATAAGGTAAAGCTAGTCTCTAACTTCCAGGCCCA  
CGGCTCAAGTGAATTTGAATACTGCATTTACAGTGTAGAGTAACACATAA  
CATTGTATGCATGGAACATGGAGGAACAGTATTACAGTGTCTTACCCT  
CTAATCAAGAAAAGAATTACAGACTCTGATTCTACAGTGATGATTGAATT  
CTAAAAATGGTTATCATTAGGGCTTTTGATTTATAAACTTTGGGTACTT  
ATACTAAATTATGGTAGTTATTCTGCCTTCCAGTTTGCTTGATATATTTG  
TTGATATTAAGATTCTTGACTTATATTTTGAATGGGTTCTAGTGAAAAAG  
GAATGATATATTTCTGAAACATCGATATACATTTATTTTAACTCTTGAT  
TCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGGTGATAAAAG  
TCACGTGAAACAGAGTGATTGGTTGCATCCAGGCCTTTTGTCTTGGTGT  
CATGATCTCCCTCTAAGCACATTCCAAATTTAGCAACAGTTATCACACT  
TTGTAATTTGCAAAGAAAAGTTTACCTGTATTGAATCAGAATGCCTTCA  
ACTGAAAAAAACATATCCAAAATAATGAGGAAATGTGTTGGCTCACTACG  
TAGAGTCCAGAGGACAGTCAGTTTTAGGGTTGCCTGTATCCAGTAACTC  
GGGGCCTGTTTCCCGTGGGTCTCTGGGTGTGAGCTTTCTTTTCTCCAT  
GTGTTTGAATTTCTCCTCAGGCTGGTAGCAAGTTCTGGATCTTATACCCAA  
CACACAGCAACATCCAGAAATAAAGATCTCAGGACCCCCCAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA (SEQ ID NO:4)

FIG. 4

SV1 (>FMhxm\_44226FL01\_P1)  
MALQGISVVELSGLAPGPFCA<sup>1</sup>MLADFGARVVRVDRPGSR<sup>2</sup>YDVSRLGRGK<sup>3</sup>RS<sup>4</sup>LVL<sup>5</sup>DLKQ<sup>6</sup>P  
RGA<sup>7</sup>AVLRRLCK<sup>8</sup>RS<sup>9</sup>DV<sup>10</sup>LLEPFR<sup>11</sup>RGVMEK<sup>12</sup>LQ<sup>13</sup>LGPEILQREN<sup>14</sup>PR<sup>15</sup>LIYARLSGFGQSGS<sup>16</sup>FCRLA  
GHDINYLALSGVLSKIGRSGENPYAPLNLLADFAGGGLMCALGIIMALFD<sup>17</sup>TR<sup>18</sup>T<sup>19</sup>RGK<sup>20</sup>GQVI  
DANMVEGTAYLSSFLWKTQKSSLWEAPRGQNMLDGGAPFYTTYRTADGEFMAVGAIEPQF  
YELLIKGLGLKSDLPNQMSMDWP<sup>21</sup>EMKKK<sup>22</sup>FADVFAK<sup>23</sup>TKAEWCQIFDGTDACVTPVLTF  
EEVVHHDHNKERGSFITSEEQDVSPRPAPLLLNTPAIP<sup>24</sup>SFKRDPFIGEHTEEILEEFGFS  
REEIYQLNSDKIIESNKVKASL (SEQ ID NO:5)

14-00000

FIG. 5A

SV2 (AMACR Isoform 2; &gt;FMhxm\_44226FL02

FIG. 5B

GCAGGAGGATCACTTGAGCCCAGGAATTTGAGGCCACAGTGAATTAGGAT  
TGCACCACTGCACTCTAGCCCAGGCAACAGAACAAGAACCTGTCTCTAAA  
TAAATAAATAAAAAATAATAATAAAAAAGATGTTTTCCCTACAAAAAA  
GACTTTTCATTTGAACTCGGTCCAGCAAGGAAAATATAACCCACTCGAAG  
TCTTTAAACAGAGGAAATTTAATATAAAGAATTCCACTGGTGACGAAAG  
AGCAGAGAAGCCCAGAAGATAGTGAGGCAACCCTGATAGGAACATAACTA  
GGAAGCCAAGACCACTCCTATGGTTGCAGGGGTGATGGGAAAGCTGGTGT  
ACTTGGACCCAGAAGCCAAAGTTGCTGCACCCACCTGGAGACATAGACA  
CTGGCAGTAATACCTCAGGGAGAAGAAAGAAATCTAGGGAAATATCCTGG  
CTTCTTTCCTTCTCTCTCTCCCTAGTCTTCCTACCAGTGTCTCCCATTA  
GCCAAATCTACCTAGAAGCCAGAAAACAAGGGAACCCTGGAAATGTAGCC  
CCATAAGATAAAGAGCACCAAAGGAAATAGATCTGAGCAGACAGGCAGCA  
CAAAATGCAGTGTGTATGGTTTATTCACTCAGTAATTCCTTTAGCAAAATG  
TTTATTGAGGATCTACTAGGTGCCAGGTATCATGATACTTGCTGGGGATA  
CCATAATGAACAAAACAGACCTGTTCTCCGCTCTTGAGGAAATCAAAGAC  
AAACACAGGATATGGAATAAACCCAGAATTATCTCATTGTAAAATGTGTT  
AAGTACCACGAGGAGAAATATCAGGGCCATCTGACACAGCTAATGATTTG  
AAGAAGGGTGTGACCTGCCACCATTTTAAATCTAGTTATTTCACTCCTGA  
GCTGTGTGTGTGGAAAACCTGTAGTAAAAAATAGAATGTCTATATTTATA  
AAAAGTTTATGAAAAGATATCAATTTATTTACATTTTGACAACTCTATG  
TAATAAGGCTTTTATTACTCACGGCCATGTGTGTGATCATGTGTAATAGCA  
TGTGTGTATGAGAGAGAGAAGCCATATGTAATTATGTGTAATAACGTCTG  
TGAGAGAGAAGCCATGTGTGTGATCATGTAAAATAACGTGTGTGAGAGAA  
GCCATGTGTGTGATCGTGTAAAATAACGTGTGTGAGAAGCCGTGTGTGAT  
GTGT (SEQ ID NO:6)

09957303-092601

FIG. 6

SV2 (&gt;FMhXm\_44226FL02\_P1)

MALQGISVVELSGLAPGPF CAMVLADFGARVVRVDRPGSR YDVSRLGRGKRS LVLDLKQP  
RGA AVLRLRLCKRSDV LLEPFRRGVMEKLQLGPEILQRENPR LIYARLSGFGQSGSFCRLA  
GHDINYLALSGVLSKIGRSGENPYAPLNL LADFAGGGLMCALGIIMALFDRTRTDKGQVI  
DANMVEGTAYLSSFLWKTQKSSLWEAPRGQNMLDGGAPFYTTYRTADGEFMAVGAIEPQF  
YELLIKGLGLKSDLPNQMSMDWPEMKKKFADVFAKTKAEWCQIFDGTDACVTPVLTF  
EEVVHHDHNKERGSFITSEEQDVSPRPAPLLLNTPAIPSKRDPFIGEHTEEILEEFGFS  
REEIYQLNSDKIIESNKAGSKFWILYPHTSNIQK (SEQ ID NO:7)

**PLATE 2**

[illegible]

GGGCGCCGGGATTGGGAGGGCTTCTTGCAGGCTGCTGGGCTGGGGCTAAG  
GGCTGCTCAGTTTCCCTCAGCGGGGCACTGGGAAGCGCCATGGCACTGCA  
GGGCATCTCGGTCGTGGAGCTGTCCGGCCTGGCCCCGGGCCCCGTTCTGTG  
CTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCC  
GGCTCCCGCTACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGT  
GCTGGACCTGAAGCAGCCGCGGGGAGCCGCCGTGCTGCGGCGTCTGTGCA  
AGCGGTTCGGATGTGCTGCTGGAGCCCTTCCGCCGCGGTGTATGGAGAAA  
CTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAAATCCAAGGCTTATTTA  
TGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTC  
GCCACGATATCAACTATTTGGCTTTGTCAAGGTGGAAGGAACAGCATATTT  
AAGTTCCTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTC  
GAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGG  
ACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCACCGATTCTA  
CGAGCTGCTGATCAAAAGGACTTGGACATAAGTCTGATGAACCTCCCAATC  
AGATGAGCATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTA  
TTTGCAAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGA  
TGCCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATC  
ACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGC  
CCCCGCCCTGCACCTCTGCTGTTAAACACCCCAGCCATCCCTTCTTTCAA  
AAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTG  
GATTACAGCCGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAA  
AGTAATAAGGTAAAAGCTAGTCTCTAACTTCCAGGCCCCAGGCTCAAGTG  
AATTTGAATACTGCATTTACAGTGTAGAGTAACACATAACATTGTATGCA  
TGGAACCATGGAGGAACAGTATTACAGTGTCTTACCACCTCTAATCAAGAA  
AGAATTACAGACTCTGATTCTACAGTGATGATTGAATTCTAAAAATGGT  
TATCATTAGGGCTTTTGATTATAAACTTTGGGTACTTATACTAAATTA  
TGGTAGTTATTCTGCCTTCCAGTTTGCTTGATATATTTGTTGATATTAAG  
ATTCTTGACTTATATTTTGAATGGGTTCTAGTGAAAAAGGAATGATATAT  
TCTTGAAGACATCGATATACAACTTATTACACTCTTGATTCTACAATGTA  
GAAAATGAGGAAATGCCACAATTTGATGGTGATAAAAGTCACGTGAAAC  
AGATGATTGGTTGTCATCCAGGCCTTTTGTCTTGGTGTTTCATGATCTCCC  
TCTAAGCACATTCCAACTTTAGCAACAGTTATCACACTTTGTAATTTGC  
AAAGAAAAGTTTCACCTGTATTGAATCAGAATGCCTTCAACTGAAAAAAA  
CATATCCAAAATAATGAGGAAATGTGTTGGCTCACTACGTAGAGTCCAGA  
GGGACAGTCAGTTTTAGGGTTGCCTGTATCCAGTAACCTCGGGGCTGTTT  
CCCCGTGGGTCTCTGGGCTGTGAGCTTTCCTTCTCCATGTGTTTGATT  
CTCCTCAGGCTGGTAGCAAGTTCTGGATCTTATACCCAACACACAGCAAC  
ATCCAGAAATAAAGATCTCAGGACCCCCCAGCAAGTCGTTTTGTGCTCC  
TTGGACTGAGTTAAGTTACAAGCCTTTCTTATACCTGTCTTTGACAAAGA  
AGACGGGAATTGCTTTTACATAAAACCAGCCTGCTCCTGGAGCTTCCCTGG  
ACTCAACTTCCTAAAGGCATGTGAGGAAGGGGTAGATTCCACAATCTAAT  
CCGGGTGCCATCAGAGTAGAGGGAGTAGAGAATGGATGTTGGGTAGGCCA  
TCAATAAGGTCCATTCTGCGCAGTATCTCAACTGCCGTTCAACAATCGCA  
AGAGGAAGGTGGAGCAGGTTTCTTCATCTTACAGTTGAGAAAAACAGAGAC  
TCAGAAGGGCTTCTAGTTTCATGTTTCCCTTAGCGCCTCAGTGATTTTTT  
CATGGTGGCTTAGGCCAAAAGAAATATCTAACATTCAATTTATAAATAA  
TTAGGTCCCCAACGAATTAATAATTATGTCTTACCAACTTATTAGCTGCT  
TGAAAAATATAATACACATAAATAAAAAAATATATTTTTTCATTTCTATTT  
CATTTGTTAATCACAACTACTTACTAAGGAGATGTATGCACCTATTGGACA



FIG. 7B

CTGTGCAACTTCTCACCTGGAATGAGATTGGACACTGCTGCCCTCATTTT  
CTGCTCCATGTTGGTGTCCATATAGTACTTGATTTTTTATCAGATGGCCT  
GGAAAACCCAGTCTCACAAAAATATGAAATTATCAGAAGGATTATAGTGC  
AATCTTATGTTGAAAGAATGAACTACCTCACTAGTAGTTCACGTGATGTC  
TGACAGATGTTGAGTTTCATTGTGTTTGTGTGTTCAAATTTTTAAATATT  
CTGAGATACTCTTGTGAGGTCACCTCTAATGCCCTGGGTGCCTTGGCACAG  
TTTTAGAAATACCAGTTGAAAATATTTGCTCAGGAATATGCAACTAGGAA  
:GGGGCAGAATCAGAATTTAAGCTTTTCATATCTAGCCTTCAGCTTGT  
CTTCAACCATTTTTAGGAACCTTTCCCAAGGTTATGTTTTCCAGCCAG  
GCATGGAGGATCACTTGAGGCCAAGAGTTCGAGACCAGCCTGGGGAACTT  
GGCTGGACCTCCGTTTTCTACGAAATAAAAAATAAAAAATTATCCAGGAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:8)

FIG. 8

SV3 (&gt;FMhxm\_44226FL03\_P1)

MALQGISVVELSGLAPGPF CAMVLADFGARVVRVDRPGSR YDVSRLGRGKRS LVLDLKQP  
RGA AVLRR LCKRSDV LLEPFRRGVMEKLQLGPEILQRENPR LIYARLSGFGQSGSFCRLA  
GHDINYLALSGGRNSIFKFFSVENSEIESVGSTSRTEHVGWWSTFLYDLQDSRWGIHGCW  
SNRTPVLRAADQRTWKV (SEQ ID NO:9)

**SECRET**

[illegible]

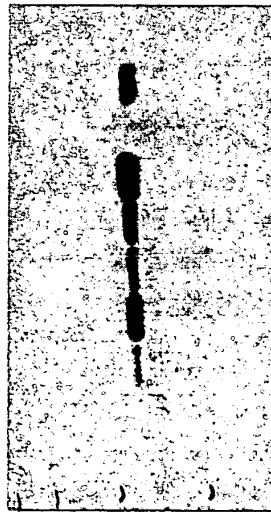
TTGACAGGCTGCTGGGCTGGGGCTAAGGGCTGCTCAGTTTCCTTCAGCGGG  
GCACTGGGAAGCGCCATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTG  
CGGCCTGGCCCCGGGCCCGTTCTGTGCTATGGTCCTGGCTGACTTCGGGG  
CGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGC  
TTGGGCCCGGGGCAAGCGCTCGCTAGTGCTGGACCTGAAGCAGCCGCGGGG  
AGCCGCCGTGCTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGCTGGAGC  
CCTTCCGCCCGGGTGTGATGGAGAACTCCAGCTGGGCCAGAGATTCTG  
CAGCGGGAAAATCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCA  
GTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT  
GTGTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAGAATCCGTATGCC  
CCGCTGAATCTCCTGGCTGACTTTTGCTGGTGGTGGCCTTATGTGTGCACT  
GGGCATTATAATGGCTCTTTTTGACCGCACACGCACTGGCAAGGGTCAGG  
TCATTGATGCAAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTG  
TGGAAAATCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAAAT  
GTTGGATGGTGGAGCACCCTTTCTATACGACTTACAGGACAGCATGGGG  
AATTCATGGCTGTTGGAGCAATAGAACCCCACTTCTACGAGCTGCTGATC  
AAAGGACTTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGA  
TGATTGGCCAGAAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAGAAGA  
CGAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACT  
CCGTTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACAACAAGGAACG  
GGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCCCTGCAC  
CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAGGGATCCTTTC  
ATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATTTCAGCCGCGA  
AGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAA  
AAGCTAGTCTCTAACTTCCAGGCCCCACGGCTCAAGTGAATTTGAATACTG  
CATTTACAGTGTAGAGTAACACATAACATTGTATGCATGGAAACATGGAG  
GAACAGTATTACAGTGTCTTACCCTCTAATCAAGAAAAGAATTACAGAC  
TCTGATTCTACAGTGATGATTGAATTCTAAAAATGGTTATCATTAGGGCT  
TTTGATTTTATAAACTTTGGGTACTTATACTAAATTATGGTAGTTATTCT  
GCCTTCCAGTTTGCTTGATATATTTGTTGATATTAAGATTCTTGACTTAT  
ATTTTGAATGGGTTCTAGTGAAAAAGGAATGATATATTCTTGAAGACATC  
GATATACATTTATTTACACTCTTGATTCTACAATGTAGAAAATGAGGAAA  
TGCCACAAATTGTATGGTGATAAAAGTCACGTGAAACAGAGTGATTGGTT  
GCATCCAGGCCTTTTGTCTTGGTGTTCATGATCTCCCTCTAAGCATTTC  
CAAACCTTTAGCAACAGTTATCACACTTTGTAATTTGCAAAAGAAAAGTTTC  
ACCTGTATTGAATCAGAATGCCTTCAACTGAAAAAACATATCCAAAATA  
ATGAGGAAATGTGTTGGCTCACTACGTAGAGTCCAGAGGGACAGTCAGTT  
TTAGGGTTGCTGTATCCAGTAACTCGGGGCCTGTTTCCCCGTGGGTCTC  
TGGGCTGTGAGCTTTTCTTTCTCCATGTGTTTGATTTCTCCTCAGGCTGG  
TAGCAAGTTCTGGATCTTATACCCAACACACAGCAACATCCAGAAATAAA  
GATCT (SEQ ID NO:10)

MALQGISVVELSGLAPGPF CAMVLADFGARVVRVDRPGSRYDVSRLGRGKRSVLVDLQKP  
RGAAVLRRRLCKRSDVLLLEPFRRGVMEKLQLGPEILQRENPRLIYARLSGFGQSGSFCRLA  
GHDINYLA LSGVLSKIGRSGENPYAPLNLLADFAGGGLMCALGIIMALFDRTRTGKGQVI  
DANMVEGTAYLSSFLWKTQKSSLWEAPRGQNMLDGGAPFYTTYRTADGEFMAVGAIEPQF  
YELLIKGLGLKSDLPNQMSMDWPENKKKFADVFAKKTAEWCQIFDGTDACVTPVLTF  
EEVVHHDHNKERGSFITSEEQDVSPRPAPLLLNTPAIPSFKRDPFIGEHTEEILEEFGFS  
REEIYQLNSDKIESNKVKASL (SEQ ID NO:11)

1002260" 50E/9660

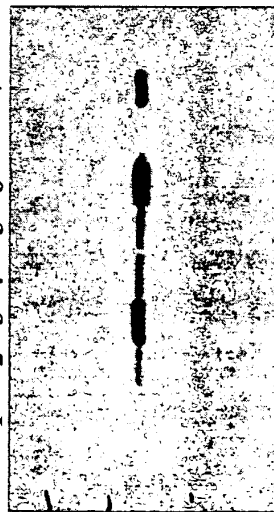
- |                            |                         |
|----------------------------|-------------------------|
| 1) normal prostate         | 7) normal colon         |
| 2) prostate adenocarcinoma | 8) colon adenocarcinoma |
| 3) prostate adenocarcinoma | 9) liver met (colon)    |
| 4) lymph node met (prost)  | 10) normal liver        |
| 5) liver met (prost)       | 11) normal kidney       |
| 6) liver met (prost)       | 12) normal kidney       |
|                            | 13) normal brain        |
|                            | 14) normal muscle       |
|                            | 15) normal muscle       |

1 2 3 4 5 6 + 7 8 9 10 11 12 13 14 15



ML 185

1 2 3 4 5 6 + 7 8 9 10 11 12 13 14 15



ML 186

FIG. 11

FIG. 12

# Racemate splice variants identified by sequencing of IMAGE clones

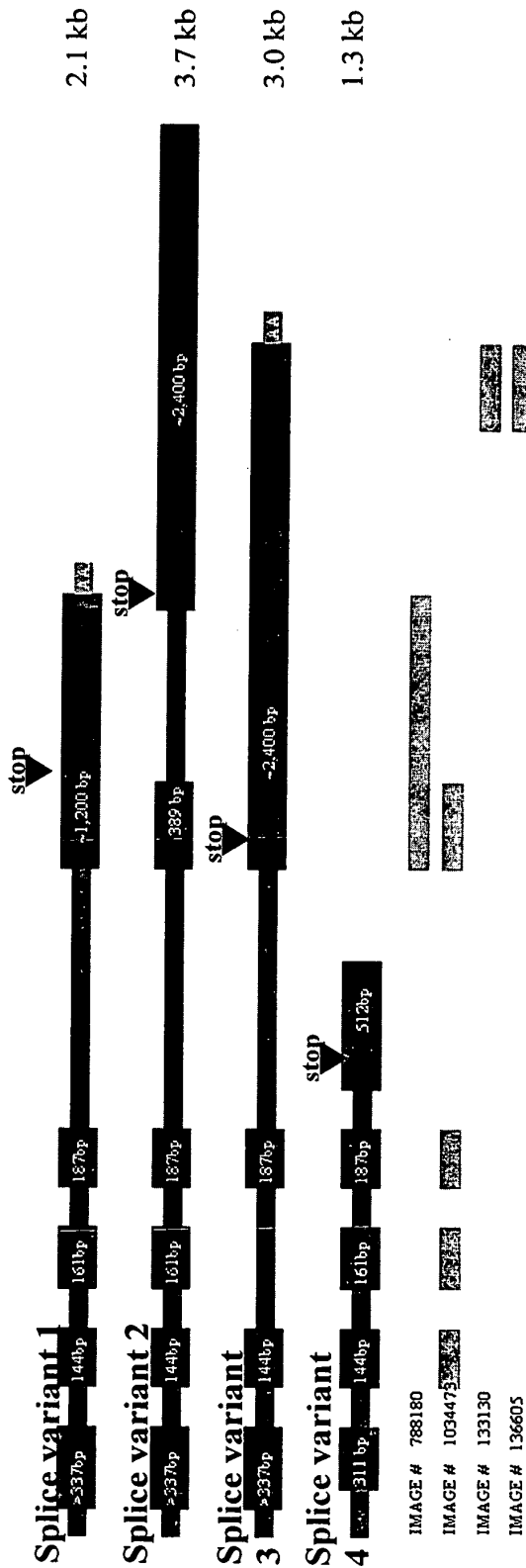
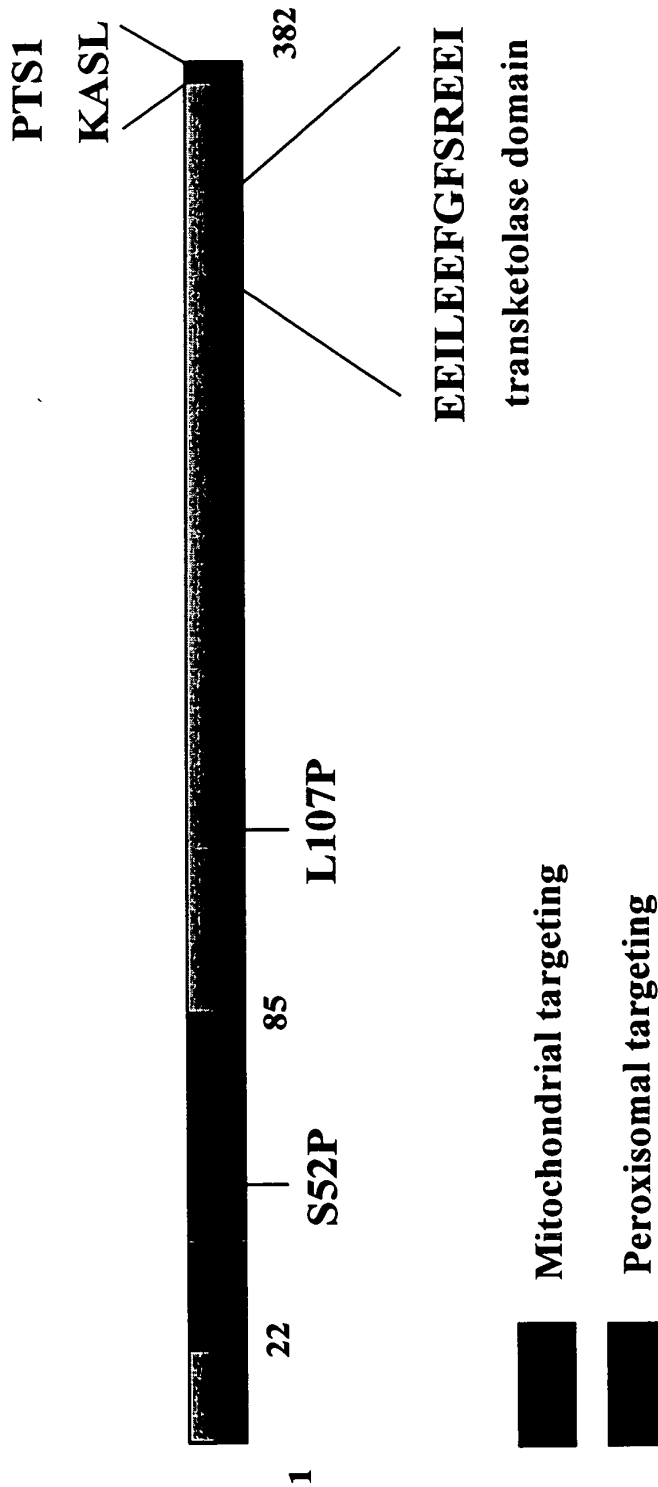


FIG. 13



TOP SECRET 50E/5660

IMAGE clone 136605

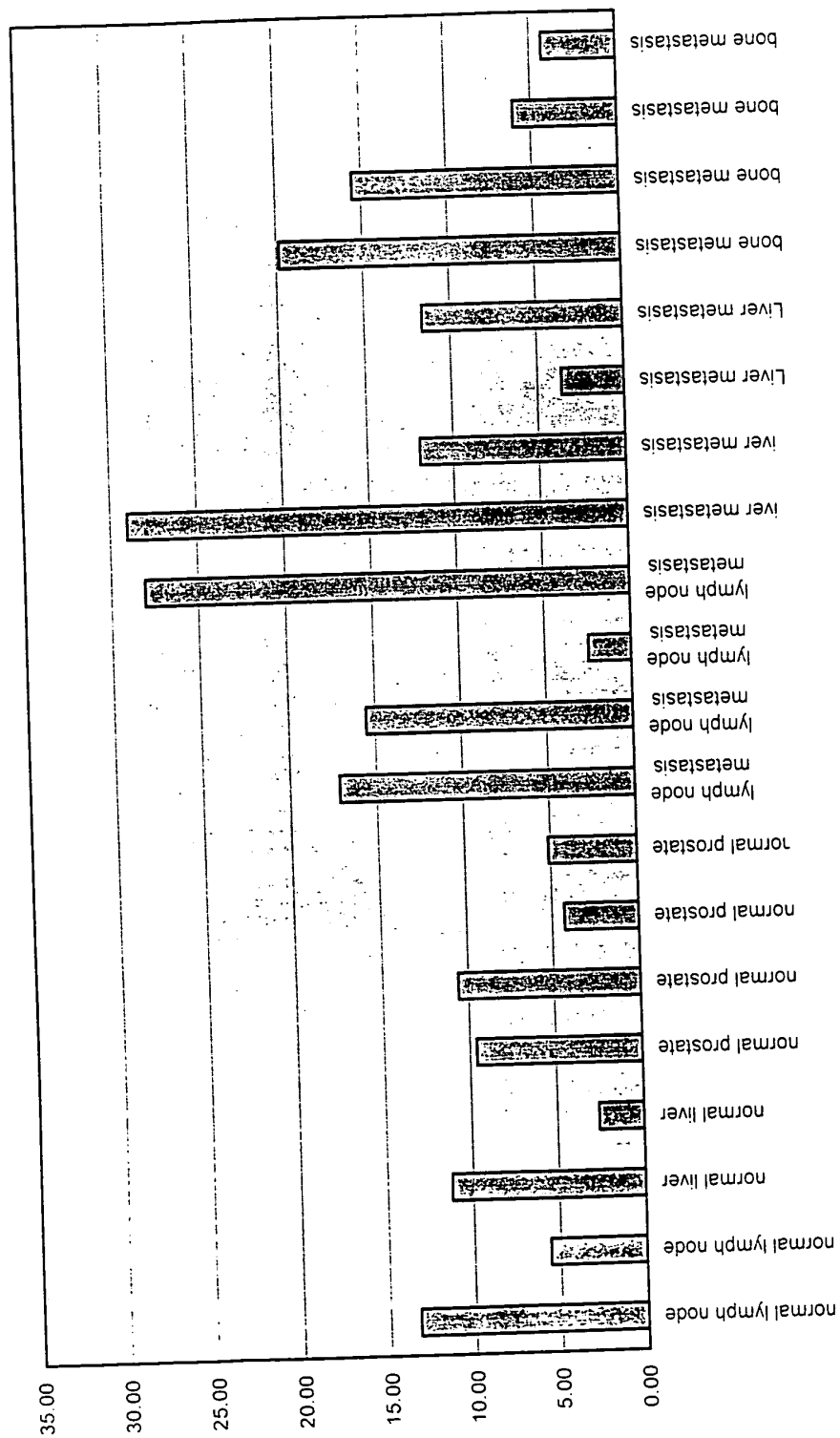


FIG. 14A



108260 502/9660

IMAGE clone 133130

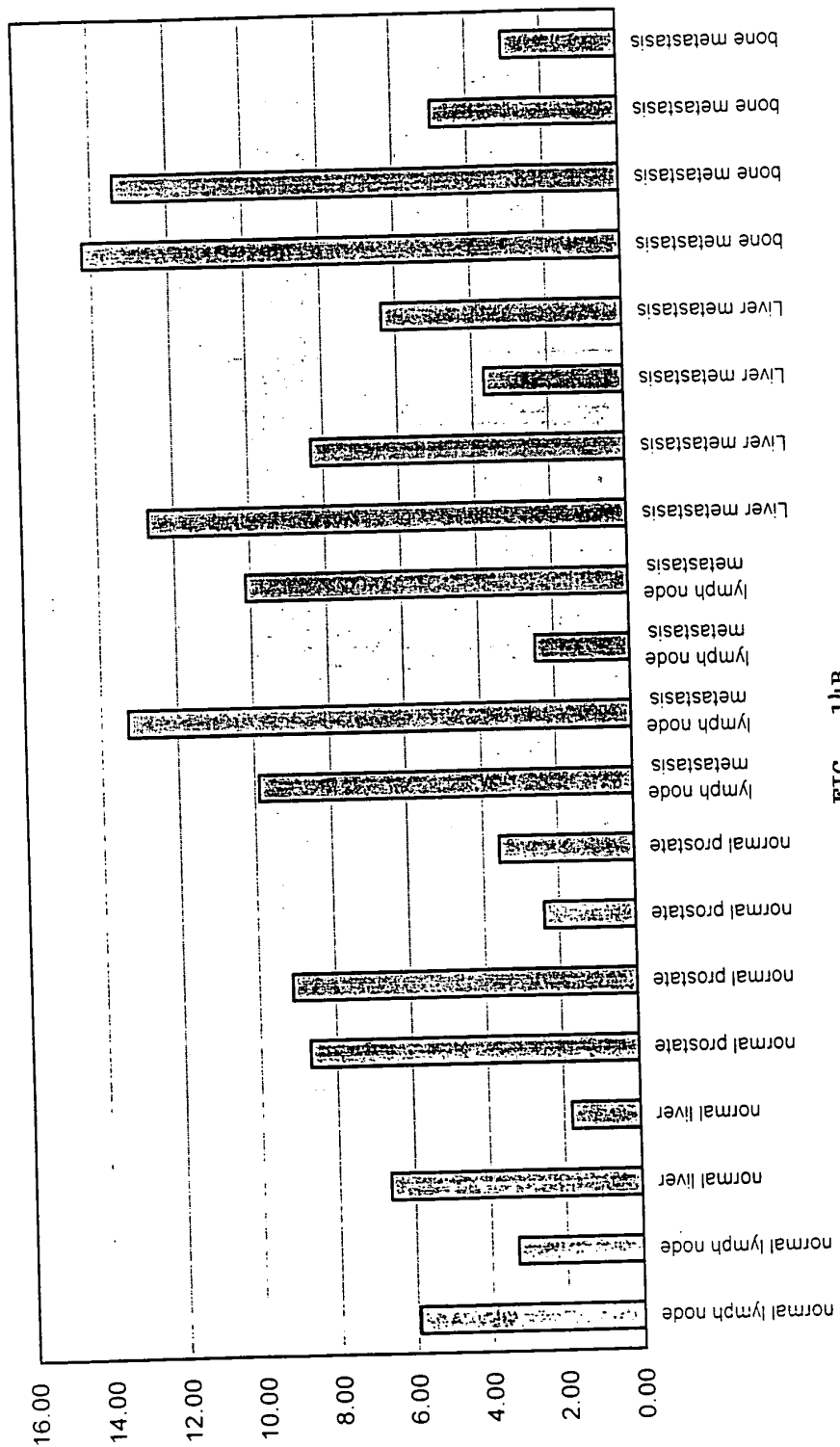


FIG. 14B

1034473 "502/9660"

IMAGE clone 1034473: MID=44226 alpha-methylacyl-CoA racemase

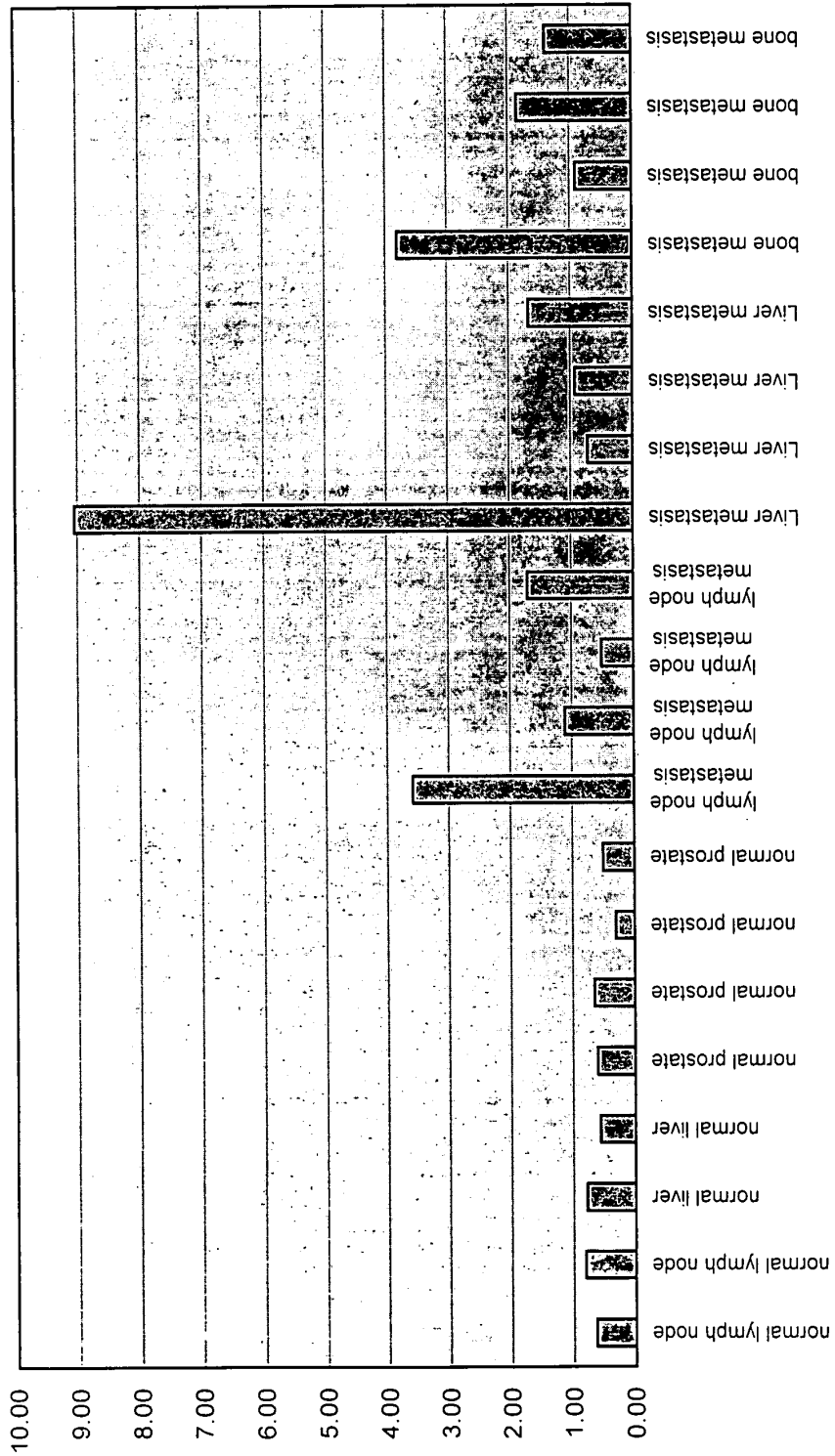


FIG. 14C

703667-9660

IMAGE clone 788180: MID=44226 alpha-methylacyl-CoA racemase

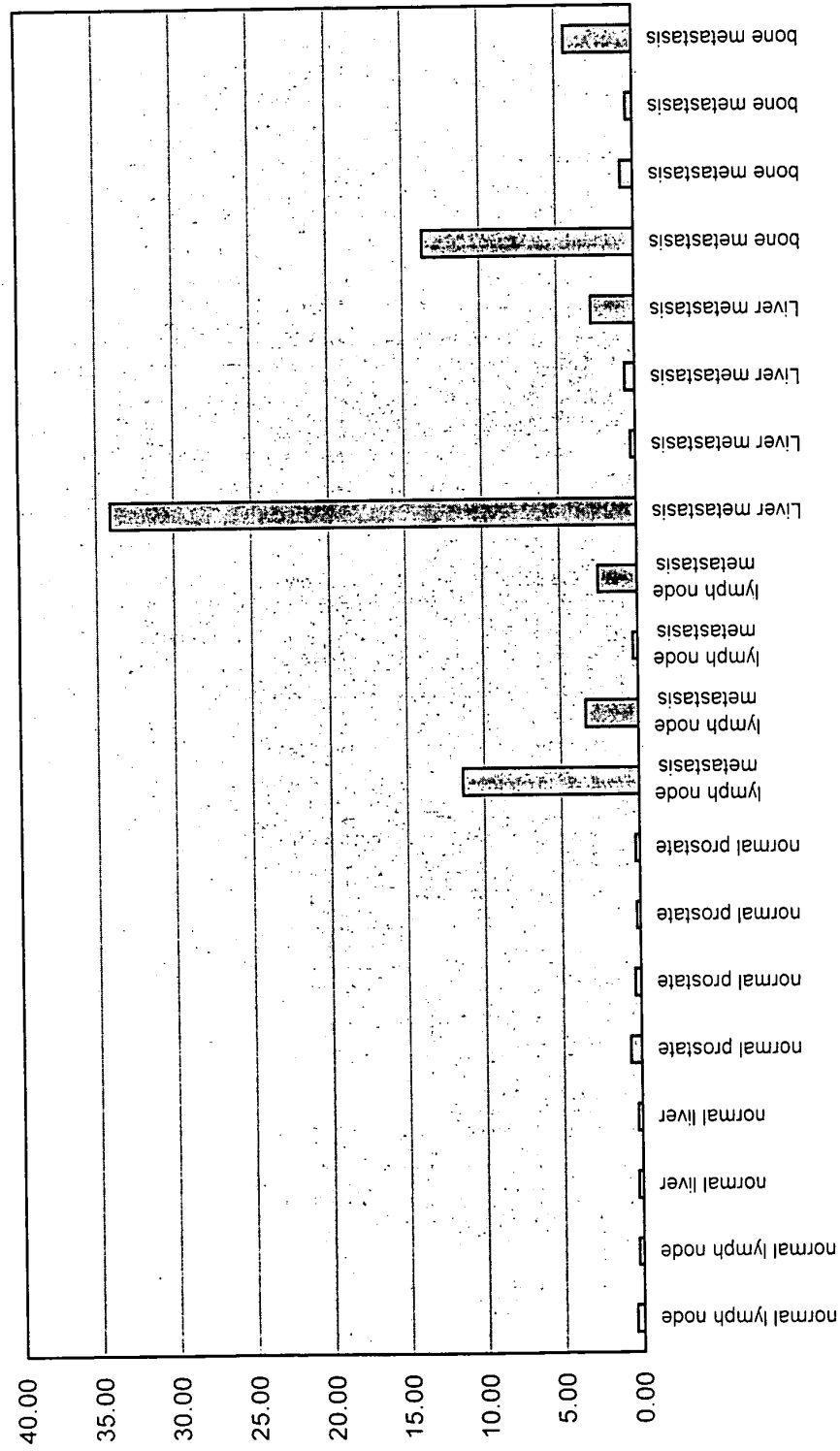


FIG. 14D